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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/735, A61K 38/17		A2	(11) International Publication Number: WO 96/34953
			(43) International Publication Date: 7 November 1996 (07.11.96)
(21) International Application Number: PCT/IB96/00590		(81) Designated States: AU, CA, JP, KR, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
(22) International Filing Date: 3 May 1996 (03.05.96)			
(30) Priority Data: 08/433,123 3 May 1995 (03.05.95) US		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
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(54) Title: CD16-II VARIANTS			
(57) Abstract			
<p>Human CD16-II variants, DNA sequences coding for them, their use in therapy and/or in diagnosis of autoimmune diseases and inflammatory illnesses, as well as pharmaceutical compositions comprising them, are disclosed. The sequence listing for the new polypeptides is provided.</p>			
<p>Application No.: 10/756,153 Attorney Docket No.: 13783-105015 References B3</p>			

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GA	Gabon			VN	Viet Nam

CD16-II VARIANTS**FIELD OF THE INVENTION**

The present invention relates to human CD16-II
5 protein variants, DNA sequences coding for them, their use in
therapy and/or in diagnosis of autoimmune diseases and
inflammatory illnesses, as well as pharmaceutical compositions
comprising them.

BACKGROUND OF THE INVENTION

10 CD16, also called Fc γ receptor-III (Fc γ R-III), is a
low affinity receptor for Immunoglobulin G (IgG). With other
receptors of the immunoglobulin Fc portion (Fc γ R-I, Fc γ R-II,
Fc ϵ R-I), CD16 plays an important role in mediating autoimmunity
and inflammatory responses.

15 Studies using monoclonal antibodies against CD16 have
established this receptor's role in removing immune complexes
from circulation and in mediating antibody-dependent cell
mediated cellular cytotoxicity (ADCC) (see for example Van de
Winkel et al., Immunol. Today, 14, 1993, pp.215-221). The
20 binding of IgG with CD16 elicits NK/LGL cell activation and
triggers ADCC. ADCC can be halted in the presence of high
levels of soluble CD16.

It has been found (see Mathiot et al., J. Clin.
Immunol., 13, (1), 1993, pp. 41-8) that the level of soluble
25 CD16 was significantly decreased in patients with multiple
myeloma compared with healthy volunteers. In addition a
stage-dependent decrease of soluble CD16 was observed, with a
highly significant difference between stage I and stages II +
III myeloma patients. Therefore the measurement of soluble
30 CD16 in serum is both a diagnostic and a prognostic marker of
myeloma, which can be useful to define and guide novel
immunomodulatory therapies of the disease.

It has further been found that CD16 is present in
human serum and other body fluids and is elevated at sites of
35 inflammation (see Fleit et al., Blood, 79, (10), 1992, pp.
2721-8).

From Ravetch et al. (J. Exp. Med., 170, 1989, pp.
481-97) it is clear that there are at least two isoforms of
human CD16, type 1 and type 2, that can be designated as CD16-I
40 and CD16-II, respectively. These two isoforms of CD16 are

- 2 -

human CD16, type 1 and type 2, that can be designated as CD16-I and CD16-II, respectively. These two isoforms of CD16 are encoded by two separate but related genes, NA1 and NA2.

From Scallan et al. (PNAS USA, 86, pp.5079-83, July 5 1989) it is evident that CD16-I and CD16-II are distinct in both structure and cellular expression. CD16-I is expressed predominantly on the surface of neutrophils and monocytes, whereas CD16-II is expressed predominantly on the surface of macrophages, natural killer cells and large granular 10 lymphocytes (NK/LGL). Furthermore, these two types of CD-16 are associated with the cell surface via two distinct mechanisms: CD16 type I is associated with the cell surface by glycosyl-phosphatidylinositol (GPI) linkage; whereas CD16 type II is anchored on the membrane with about 20 extra amino acids. 15 Furthermore, the N-terminus of the mature CD16 has been investigated and the methionine residue at position 18 was identified as the N-terminal residue of the mature protein. Thus, the initial translation product contains a 17-amino acid signal peptide. The transmembrane region of CD16-II is shown 20 to be from amino acid 209 to 229, whereas CD16-I is reported lacking transmembranal and cytoplasmic domains.

It has been determined that a single amino acid at position 203, Ser, found in isoform I versus Phe, found in type II, determines the membrane anchoring mechanism (see Lanier et 25 al., Science, 246, 1989, pp. 1611-3).

For human CD16-I, a polymorphism has been reported previously, as is evident from Figure 1, whereas only one alternative nucleic acid sequence encoding CD16-II has been published until now (Ravetch et al., J. Exp. Med., 170, 1989, 30 pp. 481-97).

Recently, Huizinga et al. (see Blood, 76, pp. 1927-, 1990) published evidence that CD16-I deficiency is related to neonatal isoimmune neutropenia.

Bredius et al. (in Immunology, 83, pp. 624-, 1994) 35 reported specifically that CD16-I-NA1 exhibited a 21-25% higher IgG1 mediated phagocytosis than CD16-I-NA2.

It has been reported that circulating levels of soluble CD16 are reduced in Multiple Myeloma, and an inhibitory

- 3 -

effect of sCD16 on myeloma cells and pokeweed mitogen (PWM)
-induced B-cell proliferation have been reported (see,
respectively, Hoover et al., J. Cli. Inve., 95(1), pp.241-7,
1995) and Teillaud et al., Blood, 82(10), 15 Nov.1993).

5 European Patent Application EP 343 950 generally
discloses soluble and membrane-bound human Fc γ R-III
polypeptides as well as nucleic acids capable of encoding the
same. In particular, the sequence of a CD16-I variant and the
sequence of CD16-II are shown in the Figures. This patent
10 application further discloses various utilities for these
polypeptides.

Citation of any document herein is not intended as an
admission that such document is pertinent prior art, or
considered material to the patentability of any claim of the
15 present application. Any statement as to content or a date of
any document is based on the information available to applicant
at the time of filing and does not constitute an admission as
to the correctness of such a statement.

20 **SUMMARY OF THE INVENTION**

The present invention is based on the discovery of
new human CD16-II variant clones. They have been isolated by
using an RT-PCR (Reverse Transcriptase-Polymerase Chain
Reaction) -based strategy using designed isoform-specific
25 oligonucleotide primers. In particular, from a pooled human
lung RNA extract, CD16-II has been amplified via RT-PCR. These
CD16-II variants provide a therapeutic intervening approach
and/or a diagnostic tool for autoimmune and inflammatory
diseases. As they are natural variants of the CD16-II sequence
30 previously published, the polypeptides of the present invention
can be used for any of the utilities previously disclosed for
CD16-II. All of the utilities for CD16-II made evident from
any of the publications disclosed herein are hereby
incorporated herein by reference, and particularly those in
35 European application 343,950.

The main object of the present invention are the
polypeptides comprising respectively the SEQ ID NO: 1, 2, 3 and
4.

- 4 -

Another object of the invention are the DNA molecules comprising the DNA sequences coding for each of the four polypeptides, as shown in Figure 3, including nucleotide sequences substantially the same. "Nucleotide sequences substantially the same" includes all other nucleic acid sequences which, by virtue of the degeneracy of the genetic code, also code for the given amino acid sequences. Preparation of an alternative nucleotide sequence encoding the same polypeptide but differing from the natural sequence due to changes permitted by the known degeneracy of the genetic code, can be achieved by site-specific mutagenesis of DNA that encodes an earlier prepared variant or a nonvariant version of the polypeptide of the present invention. Site-specific mutagenesis allows the production of variants through the use of specific oligonucleotide sequences that encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 20 to 25 nucleotides in length is preferred, with about 5 to 10 complementing nucleotides on each side of the sequence being altered. In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by publications such as Adelman et al., DNA, 2:183 (1983), the disclosure of which is incorporated herein by reference. As will be appreciated, the site-specific mutagenesis technique typically employs a phage vector that exists in both a single-stranded and double-stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage, for example, as disclosed by Messing et al., Third Cleveland Symposium on Macromolecules and Recombinant DNA, A. Walton, editor, Elsevier, Amsterdam (1981), the disclosure of which is incorporated herein by reference. These phage are readily available commercially and their use is generally well known to those skilled in the art. Alternatively, plasmid vectors that contain a single-stranded phage origin of replication (Veira et al., Meth. Enzymol., 153:3 (1987)) may be employed to obtain single-stranded DNA.

- 5 -

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector that includes within its sequence a DNA sequence that encodes the relevant protein. An oligonucleotide primer bearing the
5 desired mutated sequence is prepared synthetically by automated DNA/oligonucleotide synthesis. This primer is then annealed with the single-stranded protein-sequence-containing vector, and subjected to DNA-polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, to complete the synthesis of the
10 mutation-bearing strand. Thus, a mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* JM101 cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

15 As already stated, the proteins of the invention are useful in the therapy and/or diagnosis of autoimmune diseases and inflammatory illnesses. Therefore, in a further aspect, the present invention provides the use of each protein of the invention in the manufacture of a medicament for the treatment
20 of autoimmune diseases and inflammatory illnesses.

The medicament is preferably presented in the form of a pharmaceutical composition comprising one of the proteins of the invention together with one or more pharmaceutically acceptable carriers and/or excipients. Such pharmaceutical
25 compositions form yet a further aspect of the present invention.

The invention will now be described by means of the following Example, which should not be construed as in any way limiting the present invention. The Example will refer to the
30 Figures specified here below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the sequence alignment of various CD16 variants, including those of the present invention. The
35 alignment has been done by using the PC/Gene Software. The symbol "*" shows that a position in the alignment is "perfectly conserved". The symbol "." shows that a position is "well conserved". A blank space shows that a position is not

- 6 -

- conserved. "CD16I_1" is the human CD16-I aa sequence reported in Simmons et al., Nature, 333, pp. 568-570, 1988 (SEQ ID NO:5). "CD16I_2" is the human CD16-I aa sequence reported in Peltz et al., PNAS USA, 86, pp. 1013-7, 1989 (SEQ ID NO:6).
- 5 "CD16I_3" is the human CD16-I aa sequence reported in Scallan et al., PNAS USA, 86, pp. 5079-83, 1989 (SEQ ID NO:7). "CD16I_4" is the human CD16-I aa sequence reported in Lanier, Science, 246, pp. 1611-3, 1989 (SEQ ID NO:8). "FCG3 human" is the CD16-II aa sequence reported in Ravetch et al., J. Exp.
- 10 Med., 170, pp. 481-7, 1989 (SEQ ID NO:9). "CD16II_1", "CD16II_2", "CD16II_3" and "CD16II_4" are the CD16-II aa sequences of the proteins of the present invention respectively SEQ ID NO: 1, 2, 3 and 4.

- Figure 2 illustrates the reverse transcriptase based
- 15 polymerase chain reaction (RT-PCR) amplification of human CD16. Panel A shows the isoform-specific oligonucleotide PCR primers. The primers on the line marked "Type I" (CD16p1 (nucleotides 7-21 of SEQ ID NO:17) and CD16p5 (SEQ ID NO:11)) were designed from the published human CD16-I sequence. The primers on the
- 20 line marked "Type II" (CD16p1 (nucleotides 7-21 of SEQ ID NO:17) and CD16p6 (SEQ ID NO:12)) were designed from the human CD16-II sequence. CD16 isoform specific oligonucleotide primers for the 3' end are shown as a single mismatch at position 829, G to A. The melting temperature (T_m) of 3' PCR
- 25 primers CD16-I and CD16-II are 53.9 and 46.3°C, respectively. Panel B shows the result of restriction analysis of CD16 clones carried out using Endonuclease DraI. The banding pattern for CD16-I and CD16-II are visualised; shown on the left panel are type I clones from PCR amplification using primer pair CD16p1 and CD16p5, whereas the right panel shows type II clones from
- 30 PCR amplification using primer pair CD16p1 and CD16p6.

- Figure 3 is a comparison of the CD16-II variants of the invention in nucleic acid sequence. The first four sequences (SEQ ID NO: 12, 13, 14, and 15, respectively) are
- 35 those coding for the four variants of the present invention, whereas the last is that already known and reported in Ravetch et al., J. Exp. Med., 170, pp. 481-7, 1989 (SEQ ID NO:16). Conserved nucleotides are indicated by dashed lines, whereas

- 7 -

changed ones are spelled in lower case alphabet.

Figure 4 shows the restriction map of plasmid pcDNAI/neo-sCD16-II, useful as expression vector for CD16-II variants in CHO cells, as well as the nucleotide and amino acid sequences of the coding portion thereof (SEQ ID NOS: 17 and 18).

Figure 5 shows the restriction map of plasmid pET11(SwaI)-CD16-II, useful as expression vector for CD16-II variants in *E. coli* as well as the nucleotide and amino acid sequences of the coding portion thereof (SEQ ID NOS: 19 and 20).

EXAMPLE

15 **Enzymes and Reagents**

Human lung polyA⁺ RNA was purchased from Clontech. Moloney Murine Leukaemia Virus RNase H⁻ Reverse transcriptase (M-MLV H⁻ RT) was purchased from BRL Life Technologies, Inc. VentTM DNA polymerase, restriction endonucleases, and modifying enzymes were obtained from New England Biolabs. Sequenase Version 2.0 was purchased from US Biochemicals. The plasmid used for subcloning, pBluescript+SK, was purchased from Stratagene and used according to the manufacturer's recommendations.

25

Oligonucleotide Primer Design

To amplify CD16 type I and type II, isoform-specific oligonucleotide primers were designed as follows: 1) CD16p1: ATGTGGCAGCTGCTC (nucleotides 7-21 of SEQ ID NO:17) as 5' PCR primer for both type I and type II; 2) CD16p5 and CD16p6: CTGCTGCCACTGCTC (SEQ ID NO:21) and CTGCTGCTACTGCTC (SEQ ID NO:22) as 3' PCR primers for type I and type II, respectively. These primers were designed to amplify each isoform of CD16 specifically under a given annealing temperature, i.e., 53.9°C for type I whereas 46.3°C for type-II (Fig. 2).

Synthesis of cDNA and PCR Amplification

RNA prepared from human lung tissue was used as a

- 8 -

template for first strand cDNA synthesis. A 50 μ l reaction mixture was set up containing 2 μ Poly-A+ RNA, 2.5 μ g oligo -dT primer, 500 mM dNTPs, 50 mM Tris-HCl, pH 8.8, 75 mM KCl, 10 mM Dithiothreitol, 3 mM MgCl₂, and 100 units M-MLV H. RT. To stop the reaction, 5 ml of 500 mM EDTA was added to the mixture. The resultant mixture was extracted with an equal volume of Phenol/Chloroform/IAA (25:24:1) and precipitated with 3 volume of ethanol. The precipitated reaction was resuspended in 10 μ l of TE, and 1 ml was used for PCR amplification. PCR amplifications were performed in 100 μ l reaction mixture containing 200 μ M of dATP, dCTP, dGTP, dTTP, 10 mM KCl, 20 mM Tris-HCl, pH 8.8, 10 mM (NH₄)₂SO₄, 2 mM MgSO₄, 0.1% Triton X-100, 1 μ l of μ l (above) cDNA, and 4 units of VentTM. Thermocycles were programmed as follows: 99°C, 10-minute incubation followed by 25 cycles of 94°C, 45 seconds; 54°C for type I or 46°C for type II, 1 minute; and 75°C, 1 minute, using GeneAmp PCR System 9600 (Perkin Elmer). After agarose gel electrophoresis, resulting PCR products were extracted with phenol/chloroform, precipitated with ethanol, and digested with BamHI to yield compatible restriction ends for subcloning into pBluescript+SK or further characterization.

Characterization of CD16-II Clones

Cloning and sequencing of the PCR products were carried out following the standard molecular protocol (according to Sambrook et al., Molecular Cloning--A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989). Sequence data was analyzed using UWGCG (version 7.3) nucleic acid analysis programs following the standard protocol.

RT-PCR Amplification of CD16

Using the isoform-specific PCR primers, CD16-I and -II were amplified specifically using RT-PCR. The sequence comparison of CD16-I and CD16-II shows they are 98% identical. To amplify CD16-I, isoform-specific oligonucleotide primers were designed and used to direct PCR amplifications under specific conditions, using the cDNA generated from human lung tissue mRNA. The isoform-specific oligonucleotide primers for

- 9 -

type I and II were chosen from the 3'-untranslated region of the genes, nucleotides 822 to 836, where a single mismatch was found at nucleotide 829 (G for type-I whereas A for type-II, see Fig. 2, Panel A). Fourteen clones, picked randomly, were identified to be type I and type II by an endonuclease DraI digestion (Fig. 2, Panel B).

It was the high sequence-identity of CD16-I and -II that led to the cloning strategy of using isoform-specific oligonucleotide primers for specific isoform isolation. Due to a 98% identity in nucleotide sequence between CD16-I and CD16-II, isoform-specific oligonucleotide primers 15(mers) were designed and used to direct PCR amplifications under specific conditions (primer-template annealing temperature 54°C and 46°C for type-I and type-II, respectively). These annealing condition can stabilise the perfect match of CD16p5 to type I cDNA template at 54°C, and that of CD16p6 to type II cDNA template at a lower annealing condition, 46°C. Taking advantage of a single mismatch at nucleotide #829, according to the original cDNA numbering (Ravetch et al., *J. Exp. Med.*, 170, 1989, pp.481-7), 7 nucleotides upstream and 7 nucleotides downstream including the central nucleotide #829 (G for type-I and A for type-II), a total of 15 nucleotides were included in designing 15mers PCR primers to maintain specificity for subtype-I or -II (see Fig. 2, Panel A). As a result, subtype-I and subtype-II were isolated as shown in Panel B (Fig. 2, Panel B) and later on analyzed.

Sequence Analysis of CD16-II Clones

In addition to polymorphic variants of CD16-I, a similar type of sequence variation was found in CD16-II (see Fig 3 for nucleic acid and Fig 1 for amino acid sequences). Full length nucleotide sequence analyses were carried out and confirmed that cDNA clones for type-I contain a stop codon at 234 whereas those for type-II bear a codon for Arg at 234 and a stop codon at 255. In Fig 3, twenty-five nucleotide changes were observed. Of the 25 mismatches, 17 were found to cause codon changes (see Fig 3 and Fig 1). The remaining 8 were found to be silent mutations. Of the changes, 21 were from adenine

- 10 -

or thymine to cytosine or guanine. Four of twenty-five changes were thymine to adenine. The deduced amino acid sequence revealed that most variations found in type-I also occurred in type-II (7 of 17, see Fig 1). In addition, 10 other variations throughout the type-II translated region were observed. However, nine residues in the extracellular domain of the receptor critical for IgG binding (according to Hibbs et al., J. of Immunology, 152, 1994, pp. 4466-74), Trp131, Gln-Asn-Gly-Lys 143-146 (residues 143-146 of SEQ ID NOS:6-9), Arg-Lys-Tyr 148-150, and Gly168, remain unchanged. Interestingly, glycine at position 147 located between two important motifs Gln-Asn-Gly-Lys 143-146 (residues 143-146 of SEQ ID NOS:6-9) and Arg-Lys-Tyr 148-150, was found changed to an aspartic acid, a conserved change. Apparently, glycine 147 can be mutated to, at least, alanine without severely altering the IgG binding property. Lastly, in one of the four variants of CD16-II there was a mutation observed in the putative transmembrane domain, Val214 to Ala, a conserved change. However, a motif Leu-Phe-Ala-Val-Asp-Thr-Gly-Leu (residues 218-225 of SEQ ID NOS:6-9) in the transmembrane domain was found identical to the previously reported sequence. And this amino acid motif was found completely conserved through human and mouse CD16 and human, mouse, and rat FcεRIa.

25 Genetic Engineering of CD16-II Variants for Expression in CHO Cells and *E. coli*

The following procedures are applicable for the expression and purification of each of the CD16-II variants of the invention, even though CD16-II, generically, will be mentioned.

In order to engineer soluble CD16-II (sCD16-II) for CHO expression, oligonucleotide primer CD16p14 is designed as GGGGAATTCAAAGAATGATGAGATGGT (SEQ ID NO:23). CD16p14 is designed so that a TGA stop codon is inserted after the Phe codon (Phe#203 is characteristic for CD16-II). CD16p1 and CD16p14 were used to amplify the soluble form of CD16-II (see Figure 4). The exact C terminus of the naturally occurring soluble form in CD16-II is yet to be determined; however, by

- 11 -

choosing this truncation the engineered form of soluble CD16-II will contain the extracellular portion of the molecule.

For *E. coli* expression of sCD16-II, oligonucleotide primers, CD16-(SwaI) and CD16N233, are designed as

5 TTTGGATCCAAGCTTAGTTTGTCTTCACAGAGAAATAGAGACCT (SEQ ID NO:24) and
TTTATTTAAATGCGTACTGAAGATCTCCCAAAG (SEQ ID NO:25), respectively.

CD16-(SwaI) and CD16N233 primers are designed so that in *E. coli*, amino acid sequence from #18 to #233 (see Figure 5) could be produced, which is the mature protein, also containing
10 the transmembranal domain.

Methotrexate (MTX) amplification is used in CHO cell expression of CD16-II.

Large scale DNA preparation of plasmid pcDNAI/neo-sCD16-II (see Figure 4) is carried out using Qiagen column
15 followed by ethanol precipitation and was used for stable transfection by cotransfecting with D α vector (containing the DHFR gene) for MTX selection. CHO transfectants are pooled and fully amplified to 5 μ M MTX. In order to produce sCD16 for purification, the highest sCD16 producing pool is selected and
20 cultured in MTX-free basal medium (JRH, Biosciences) or MTX-free low protein medium (SFM-II, Gibco). The culture medium is collected at 24, 48 or 72 hours and used for purification on IgG affinity chromatography. Analysis of sCD16-II is done using OD₂₈₀, SDS-PAGE, ELISA, Western blotting,
25 amino acid composition analysis and N-terminal sequencing.

For *E. coli* expression of sCD16-II, isopropylthio- β -galactoside (IPTG) induced BL21/DE3 cells are incubated in lysis buffer and the soluble material analyzed using SDS-PAGE and Western blotting with polyclonal anti-hCD16
30 antisera.

Soluble CD16-II expressed in *E. coli*, is also confirmed using N-terminal sequencing.

All references cited herein, including journal articles or abstracts, published or corresponding U.S. or
35 foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of

- 12 -

the references cited within references cited herein are also entirely incorporated by reference.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that
5 others can, by applying current knowledge, readily modify and/or adapt for various applications such specific embodiments without undue experimentation and without departing from the generic concept, and, therefore, such adaptations and modifications should and are intended to be comprehended within
10 the meaning and range of equivalents of the disclosed embodiments. The means and materials for carrying out various disclosed functions may take a variety of alternative forms without departing from the invention. It is to be understood that the phraseology or terminology employed herein is for the
15 purpose of description and not of limitation.

- 13 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LUO, Shun
- (ii) TITLE OF INVENTION: CD16-II VARIANTS
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street, N.W., Suite 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT
 - (B) FILING DATE: 03 May 1996
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/433,123
 - (B) FILING DATE: 03 May 1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWDY, Roger L.
 - (B) REGISTRATION NUMBER: 25,618
 - (C) REFERENCE/DOCKET NUMBER: LUO=2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528
 - (C) TELEX: 248633

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
1 5 10 15
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60
Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

- 14 -

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Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
      85                      90                      95
Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
      100                      105                      110
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
      115                      120                      125
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
      130                      135                      140
Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
      145                      150                      155                      160
Lys Ala Thr Leu Lys Asp Ser Gly Pro Tyr Phe Cys Arg Gly Leu Phe
      165                      170                      175
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Thr Thr Ile Thr Gln
      180                      185                      190
Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
      195                      200                      205
Val Ser Phe Cys Leu Ala Met Val Leu Leu Phe Ala Val Asp Thr Gly
      210                      215                      220
Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
      225                      230                      235                      240
Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
      245                      250

```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
1      5      10      15
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
      20      25      30
Gln Trp Tyr Ser Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
      35      40      45
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Lys Glu
      50      55      60
Asn Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
      65      70      75      80
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
      85      90      95
Ser Asp Pro Val Gln Leu Glu Val Gln Val Gly Trp Leu Leu Leu Gln
      100      105      110
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
      115      120      125

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- 15 -

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140
 Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
 145 150 155 160
 Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Lys Gly Leu Val
 165 170 175
 Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Ile Gln
 180 185 190
 Gly Leu Ala Val Ser Thr Asn Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205
 Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220
 Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
 225 230 235 240
 Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1 5 10 15
 Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30
 Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45
 Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Lys Glu
 50 55 60
 Asn Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80
 Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95
 Ser Asp Pro Val Gln Leu Glu Val Gln Val Gly Trp Leu Leu Leu Gln
 100 105 110
 Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125
 His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140
 Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
 145 150 155 160
 Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

- 16 -

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
 225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Trp Gln Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Ser His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

- 17 -

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Pro Thr Arg Asp Trp
 225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Gly Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Ser Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile
 225 230

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid

- 18 -

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1           5           10           15
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
          20           25           30
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
          35           40           45
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
          50           55           60
Asn Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
          65           70           75           80
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
          85           90           95
Ser Asp Pro Val Gln Leu Glu Val His Val Gly Trp Leu Leu Leu Gln
          100          105          110
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
          115          120          125
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
          130          135          140
Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
          145          150          155          160
Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
          165          170          175
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
          180          185          190
Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
          195          200          205
Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
          210          215          220
Leu Tyr Phe Ser Val Lys Thr Asn Ile
          225          230

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1           5           10           15
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
          20           25           30

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- 19 -

Gln Trp Tyr Ser Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45
 Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60
 Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80
 Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95
 Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110
 Ala Pro Arg Trp Val Phe Lys Glu Glu Glu Pro Ile His Leu Arg Cys
 115 120 125
 His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140
 Gly Lys Asp Arg Lys Tyr Ser His His Asn Ser Asp Phe His Ile Pro
 145 150 155 160
 Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175
 Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190
 Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
 195 200 205
 Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220
 Leu Tyr Phe Ser Val Lys Thr Asn Ile
 225 230

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
 1 5 10 15
 Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30
 Gln Trp Tyr Ser Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45
 Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60
 Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80
 Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

- 20 -

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile
 225 230

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
 1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

- 21 -

Lys	Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Phe
				165					170					175	
Gly	Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Ile	Thr	Gln
			180					185					190		
Gly	Leu	Ala	Val	Ser	Thr	Ile	Ser	Ser	Phe	Phe	Pro	Pro	Gly	Tyr	Gln
		195					200					205			
Val	Ser	Phe	Cys	Leu	Val	Met	Val	Leu	Leu	Phe	Ala	Val	Asp	Thr	Gly
		210				215					220				
Leu	Tyr	Phe	Ser	Val	Lys	Thr	Asn	Ile	Arg	Ser	Ser	Thr	Arg	Asp	Trp
225					230					235					240
Lys	Asp	His	Lys	Phe	Lys	Trp	Arg	Lys	Asp	Pro	Gln	Asp	Lys		
				245					250						

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCAGTGGC AGCAG

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCAGTAGC AGCAG

15

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGTGGCAGC	TGCTCCTCCC	AACTGCTCTG	CTACTTCTAG	TTTCAGCTGG	CATGCGGACT	60
GAAGATCTCC	CAAAGGCTGT	GGTGTTCCCTG	GAGCCTCAAT	GGTACAGGGT	GCTCGAGAAG	120
GACAGTGTGA	CTCTGAAGTG	CCAGGGAGCC	TACTCCCCTG	AGGACAATTC	CACACAGTGG	180
TTTCACAATG	AGAGCCTCAT	CTCAAGCCAG	GCCTCGAGCT	ACTTCATTGA	CGCTGCCACA	240
GTCGACGACA	GTGGAGAGTA	CAGGTGCCAG	ACAAACCTCT	CCACCCTCAG	TGACCCGGTG	300
CAGCTAGAAG	TCCATATCGG	CTGGCTGTTG	CTCCAGGCCC	CTCGGTGGGT	GTTCAAGGAG	360

- 22 -

GAAGACCCTA TTCACCTGAG GTGTCACAGC TGGAAGAACA CTGCTCTGCA TAAGGTCACA	420
TATTTCGAGA ATGGCAAAGG CAGGAAGTAT TCTCATCATA ATTCTGACTT CTACATTCCA	480
AAAGCCACAC TCAAAGACAG CGGCTCCTAC TTCTGCAGGG GGCTTTTGG GAGTAAAAAT	540
GTGTCTTCAG AGACTGTGAA CATCACCATC ACTCAAGGTT TGGCAGTGTC AACCATCTCA	600
TCATTCTTTC CACCTGGGTA CCAAGTCTCT TTCTGCTTGG TGATGGTACT CCTTTTGGCA	660
GTGGACACAG GACTATATTT CTCTGTGAAG ACAAACATTC GAAGCCCAAC AAGAGACTGG	720
AAGGACCATA AATTAAATG GAGAAAGGAC CCTCAAGGCA AATGA	765

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGTGGCAGC TGCTCCTCCC AACTGCTCTG CTACTTCTAG TTTCAGCTGG CATGAGGACT	60
GAAGATCTCC CAAAGGCTGT GGTGTTCTCTG GAGCCTCAAT GGTACAGGGT GCTCGAGAAG	120
GACAGTGTGA CTCTGAAGTG CCAGGGAGCC TACTCCCCTG AGGACAATTC CACACAGTGG	180
TTTCACAAAG AGAACCTCAT CTCAAGCCAG GCCTCGAGCT ACTTCATTGA CGCTGCCACA	240
GTCGACGACA GTGGAGAGTA CAGGTGCCAG ACGAACCTCT CCACCCTCAG TGACCCGGTG	300
CAGCTAGAAG TCCAAGTCGG CTGGCTGTTG CTCCAGGCCC CTCGGTGGGT GTTCAAGGAG	360
GAAGACCCTA TTCACCTGAG GTGTCACAGC TGGAAGAACA CTGCTATGCA TAAGGTCACA	420
TATTACAGA ATGGCAAAGA CAGGAAGTAT TTTCATCATA ATTCTGACTT CCACATTCCA	480
AAAGCCACAC TCAAAGATAG CGGCTCTTAC TTCTGCAGGG GGCTTGTGG GAGTAAAAAT	540
GTGTCTTCAG AGACTGTGAA CATCACCATC ACTCAAGGTT TGGCAGTGTC AACCATCTCA	600
TCATTCTTTC CACCTGGGTA CCAAGTCTCT TTCTGCTTGG TGATGGTACT CCTTTTGGCA	660
GTGGACACAG GACTATATTT CTCTGTGAAG ACAAACATTC GAAGCTCAAC AAGAGACTGG	720
AAGGACCATA AATTAAATG GAGAAAGGAC CCTCAAGACA AATGA	765

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGTGGCAGC TGCTCCTCCC AACTGCTCTG CTACTTCTAG TTTCAGCTGG CATGCGGACT	60
GAAGATCTCC CAAAGGCTGT GGTGTTCTCTG GAGCCTCAAT GGTACAGTGT GCTCGAGAAG	120
GACAGTGTGA CTCTGAAGTG CCAGGGAGCC TACTCCCCTG AGGACAATTC CACACAATGG	180

- 23 -

TTTCACAAAG AGAACCTCAT CTCAAGCCAG GCCTCGAGCT ACTTCATTGA CGCTGCCACA	240
GTCGACGACA GTGGAGAGTA CAGGTGCCAG ACAAACCTCT CCACCCTCAG TGACCCGGTG	300
CAGCTAGAAG TCCAAGTCGG CTGGCTGTTG CTCCAGGCCC CTCGGTGGGT GTTCAAGGAG	360
GAAGACCCTA TTCACCTGAG GTGTCACAGC TGGAAGAACA CTGCTCTGCA TAAGGTCACA	420
TATTTACAGA ATGGCAAAG CAGGAAGTAT TTTCATCATA ATTCTGACTT CCACATTCCA	480
AAAGCCACAC TCAAAGATAG CGGCTCCTAC TTCTGCAAGG GGCTTGTTGG GAGTAAAAAT	540
GTGTCTTCAG AGACTGTGAA CATCACCATC ATTCAAGGTT TGGCAGTGC AACCAACTCA	600
TCATTCTTTC CACCTGGGTA CCAAGTCTCT TTCTGCTTGG TGATGGTACT CCTTTTGTGA	660
GTGGACACAG GACTATATTT CTCTGTGAAG ACAAACATTC GAAGCTCAAC AAGAGACTGG	720
AAGGACCATA AATTTAAATG GAGAAAGGAC CCTCAAGACA AATGA	765

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGTGGCAGC TGCTCCTCCC AACTGCTCTG CTACTTCTAG TTTCAGCTGG CATGCCGACT	60
GAAGATCTCC CAAAGGCTGT GGTGTTCTCTG GAGCCTCAAT GGTACAGGGT GCTCGAGAAG	120
GACAGTGTGA CTCTGAAGTG CCAGGGAGCC TACTCCCCTG AGGACAATTC CACACAGTGG	180
TTTCACAATG AGAGCCTCAT CTCAAGCCAG GCCTCGAGCT ACTTCATTGA CGCTGCCACA	240
GTCGACGACA GTGGAGAGTA CAGGTGCCAG ACAAACCTCT CTACCCTCAG TGACCCGGTG	300
CAGCTAGAAG TCCATATCGG CTGGCTGTTG CTCCAGGCCC CTCGGTGGGT GTTCAAGGAG	360
GAAGACCCTA TTCACCTGAG GTGTCACAGC TGGAAGAACA CTGCTCTGCA TAAGGTCACA	420
TATTTACAGA ATGGCAAAGG CAGGAAGTAT TTTCATCATA ATTCTGACTT CTACATTCCA	480
AAAGCCACAC TCAAAGACAG CGGCCCTAC TTCTGCAGGG GGCTTTTGG GAGTAAAAAT	540
GTGTCTTCAG AGACTGTGAA CACCACCATC ACTCAAGGTT TGGCAGTGC AACCATCTCA	600
TCATTCTTTC CACCTGGGTA CCAAGTCTCT TTCTGCTTGG CGATGGTACT CCTTTTGTGA	660
GTGGACACAG GACTATATTT CTCTGTGAAG ACAAACATTC GAAGCTCAAC AAGAGACTGG	720
AAGGACCATA AATTTAAATG GAGAAAGGAC CCTCAAGACA AATGA	765

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 24 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGTGGCAGC TGCTCCTCCC AACTGCTCTG CTAATTCTAG TTTCAGCTGG CATGCCGACT	60
GAAGATCTCC CAAAGGCTGT GGTGTTCTCT GAGCCTCAAT GGTACAGGGT GCTCGAGAAG	120
GACAGTGTGA CTCTGAAGTG CCAGGGAGCC TACTCCCCTG AGGACAATTC CACACAGTGG	180
TTTCACAATG AGAGCCTCAT CTCAAGCCAG GCCTCGAGCT ACTTCATTGA CGCTGCCACA	240
GTCGACGACA GTGGAGAGTA CAGGTGCCAG ACAAACCTCT CCACCCTCAG TGACCCGGTG	300
CAGCTAGAAG TCCATATCGG CTGGCTGTTG CTCCAGGCCC CTCGGTGGGT GTTCAAGGAG	360
GAAGACCCTA TTCACCTGAG GTGTACACAG TGGAAGAACA CTGCTCTGCA TAAGGTCACA	420
TATTTACAGA ATGGCAAAGG CAGGAAGTAT TTTCATCATA ATTCTGACTT CTACATTCCA	480
AAAGCCACAC TCAAAGACAG CGGCTCCTAC TTCTGCAGGG GGCTTTTTTG GAGTAAAAAT	540
GTGTCTTCAG AGACTGTGAA CATCACCATC ACTCAAGGTT TGGCAGTGTC AACCATCTCA	600
TCATTCTTTC CACCTGGGTA CCAAGTCTCT TTCTGCTTGG TGATGGTACT CCTTTTGTGA	660
GTGGACACAG GACTATATTT CTCTGTGAAG ACAAACATTC GAAGCTCAAC AAGAGACTGG	720
AAGGACCATA AATTTAAATG GAGAAAGGAC CCTCAAGACA AATGA	765

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG CGG ACT GAA GAT CTC CCA AAG GCT GTG GTG TTC CTG GAG CCT CAA	48
Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln	
1 5 10 15	
TGG TAC AGG GTG CTC GAG AAG GAC AGT GTG ACT CTG AAG TGC CAG GGA	96
Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly	
20 25 30	
GCC TAC TCC CCT GAG GAC AAT TCC ACA CAG TGG TTT CAC AAT GAG AGC	144
Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser	
35 40 45	
CTC ATC TCA AGC CAG GCC TCG AGC TAC TTC ATT GAC GCT GCC ACA GTC	192
Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val	
50 55 60	
GAC GAC AGT GGA GAG TAC AGG TGC CAG ACA AAC CTC TCC ACC CTC AGT	240
Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Leu Ser Thr Leu Ser	
65 70 75 80	
GAC CCG GTG CAG CTA GAA GTC CAT ATC GGC TGG CTG TTG CTC CAG GCC	288
Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala	
85 90 95	

- 25 -

CCT CGG TGG GTG TTC AAG GAG GAA GAC CCT ATT CAC CTG AGG TGT CAC	336
Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His	
100 105 110	
AGC TGG AAG AAC ACT GCT CTG CAT AAG GTC ACA TAT TTA CAG AAT GGC	384
Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly	
115 120 125	
AAA GGC AGG AAG TAT TTT CAT CAT AAT TCT GAC TTC TAC ATT CCA AAA	432
Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys	
130 135 140	
GCC ACA CTC AAA GAC AGC GGC TCC TAC TTC TGC AGG GGG CTT TTT GGG	480
Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe Gly	
145 150 155 160	
AGT AAA AAT GTG TCT TCA GAG ACT GTG AAC ATC ACC ATC ACT CAA GGT	528
Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly	
165 170 175	
TTG GCA GTG TCA ACC ATC TCA TCA TTC TTT CCA CCT GGG TAC CAA GTC	576
Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val	
180 185 190	
TCT TTC TGC TTG GTG ATG GTA CTC CTT TTT GCA GTG GAC ACA GGA CTA	624
Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly Leu	
195 200 205	
TAT TTC TCT GTG AAG ACA AAC TAA	648
Tyr Phe Ser Val Lys Thr Asn	
210 215	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln	
1 5 10 15	
Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly	
20 25 30	
Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser	
35 40 45	
Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val	
50 55 60	
Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser	
65 70 75 80	
Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala	
85 90 95	
Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His	
100 105 110	
Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly	
115 120 125	

- 26 -

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
 130 135 140
 Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe Gly
 145 150 155 160
 Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly
 165 170 175
 Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val
 180 185 190
 Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly Leu
 195 200 205
 Tyr Phe Ser Val Lys Thr Asn
 210 215

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCC ATG TGG CAG CTG CTC CTC CCA ACT GCT CTG CTA CTT CTA GTT	48
Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val	
220 225	
TCA GCT GGC ATG CGG ACT GAA GAT CTC CCA AAG GCT GTG GTG TTC CTG	96
Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu	
230 235 240 245	
GAG CCT CAA TGG TAC AGG GTG CTC GAG AAG GAC AGT GTG ACT CTG AAG	144
Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys	
250 255 260	
TGC CAG GGA GCC TAC TCC CCT GAG GAC AAT TCC ACA CAG TGG TTT CAC	192
Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His	
265 270 275	
AAT GAG AGC CTC ATC TCA AGC CAG GCC TCG AGC TAC TTC ATT GAC GCT	240
Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala	
280 285 290	
GCC ACA GTC GAC GAC AGT GGA GAG TAC AGG TGC CAG ACA AAC CTC TCC	288
Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser	
295 300 305	
ACC CTC AGT GAC CCG GTG CAG CTA GAA GTC CAT ATC GGC TGG CTG TTG	336
Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu	
310 315 320 325	
CTC CAG GCC CCT CGG TGG GTG TTC AAG GAG GAA GAC CCT ATT CAC CTG	384
Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu	
330 335 340	
AGG TGT CAC AGC TGG AAG AAC ACT GCT CTG CAT AAG GTC ACA TAT TTA	432
Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu	
345 350 355	

- 27 -

CAG AAT GGC AAA GGC AGG AAG TAT TTT CAT CAT AAT TCT GAC TTC TAC	480
Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr	
360 365 370	
ATT CCA AAA GCC ACA CTC AAA GAC AGC GGC TCC TAC TTC TGC AGG GGG	528
Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly	
375 380 385	
CTT TTT GGG AGT AAA AAT GTG TCT TCA GAG ACT GTG AAC ATC ACC ATC	576
Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile	
390 395 400 405	
ACT CAA GGT TTG GCA GTG TCA ACC ATC TCA TCA TTC TTT TGAGAATTTCG	625
Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe	
410 415	
ATATC	630

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala	
1 5 10 15	
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro	
20 25 30	
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln	
35 40 45	
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu	
50 55 60	
Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr	
65 70 75 80	
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu	
85 90 95	
Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln	
100 105 110	
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys	
115 120 125	
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn	
130 135 140	
Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro	
145 150 155 160	
Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe	
165 170 175	
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln	
180 185 190	
Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe	
195 200	

- 28 -

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGCTGCCAC TGCTC

15

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGCTGCTAC TGCTC

15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGAATTCAA AAGAATGATG AGATGGT

27

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTTGGATCCA AGCTTAGTTT GTCTTCACAG AGAAATAGAG ACCT

44

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTATTAAA TGCCTACTGA AGATCTCCCA AAG

33

CLAIMS

1. A polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.
2. Polypeptide comprising the amino acid sequence of sequence SEQ ID No. 1.
3. Polypeptide comprising the amino acid sequence of sequence SEQ ID No. 2.
4. Polypeptide comprising the amino acid sequence of sequence SEQ ID No. 3.
5. Polypeptide comprising the amino acid sequence of sequence SEQ ID No. 4.
6. An isolated DNA molecule comprising a DNA sequence encoding a polypeptide in accordance with claim 1.
7. An isolated DNA molecule comprising a DNA sequence encoding the polypeptide of claim 2.
8. An isolated DNA molecule comprising a DNA sequence encoding the polypeptide of claim 3.
9. An isolated DNA molecule comprising a DNA sequence encoding the polypeptide of claim 4.
10. An isolated DNA molecule comprising a DNA sequence encoding the polypeptide of claim 5.
11. A method for the treatment of autoimmune diseases or inflammatory illnesses comprising administering an effective amount of a polypeptide in accordance with claim 1.
12. A method for the treatment of autoimmune diseases or inflammatory illnesses comprising administering an effective amount of a polypeptide in accordance with claim 2.
13. A method for the treatment of autoimmune diseases or inflammatory illnesses comprising administering an effective amount of a polypeptide in accordance with claim 3.
14. A method for the treatment of autoimmune diseases or inflammatory illnesses comprising administering an effective amount of a polypeptide in accordance with claim 4.
15. A method for the treatment of autoimmune diseases or inflammatory illnesses comprising administering an effective amount of a polypeptide in accordance with claim 5.

- 30 -

16. A pharmaceutical composition comprising a polypeptide in accordance with claim 1, together with one or more pharmaceutically acceptable carriers and/or excipients.

17. A pharmaceutical composition comprising the polypeptide in accordance with claim 2, together with one or more pharmaceutically acceptable carriers and/or excipients.

18. A pharmaceutical composition comprising the polypeptide in accordance with claim 3, together with one or more pharmaceutically acceptable carriers and/or excipients.

19. A pharmaceutical composition comprising the polypeptide in accordance with claim 4, together with one or more pharmaceutically acceptable carriers and/or excipients.

20. A pharmaceutical composition comprising the polypeptide in accordance with claim 5, together with one or more pharmaceutically acceptable carriers and/or excipients.

1/7

CD16I_1	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYSVLEK	40
CD16I_4	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYSVLEK	40
CD16I_3	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYSVLEK	40
CD16I_2	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYRVLEK	40
FCG3_HUMAN	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYRVLEK	40
CD16II_1	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYRVLEK	40
CD16II_4	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYRVLEK	40
CD16II_2	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYSVLEK	40
CD16II_3	MWQLLLPTALLLLVSAGMRTE	LPKAVVFLEPQWYRVLEK	40
*****.****			
CD16I_1	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16I_4	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16I_3	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16I_2	DSVTLKCQGAYSPEDNSTQWFHNE	NLISSQASSYFIDAAT	80
FCG3_HUMAN	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16II_1	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16II_4	DSVTLKCQGAYSPEDNSTQWFHNE	SLISSQASSYFIDAAT	80
CD16II_2	DSVTLKCQGAYSPEDNSTQWFHNE	KENLISSQASSYFIDAAT	80
CD16II_3	DSVTLKCQGAYSPEDNSTQWFHNE	KENLISSQASSYFIDAAT	80
*****.*.*****			
CD16I_1	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16I_4	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16I_3	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16I_2	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
FCG3_HUMAN	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16II_1	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16II_4	VNDSGEYRCQTNLSTLSDPVQLEV	HIGWLLLQAPRWVFKE	120
CD16II_2	VNDSGEYRCQTNLSTLSDPVQLEV	QVGWLLLQAPRWVFKE	120
CD16II_3	VNDSGEYRCQTNLSTLSDPVQLEV	QVGWLLLQAPRWVFKE	120
*.*****.*****			
CD16I_1	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYFHHNSDFHIP	160
CD16I_4	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYFHHNSDFHIP	160
CD16I_3	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYSHHNSDFHIP	160
CD16I_2	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYFHHNSDFHIP	160
FCG3_HUMAN	EDPIHLRCHSWKNTALHKVTTYLQ	NGKGRKYFHHNSDFYIP	160
CD16II_1	EDPIHLRCHSWKNTALHKVTTYLQ	NGKGRKYFHHNSDFYIP	160
CD16II_4	EDPIHLRCHSWKNTALHKVTTYLQ	NGKGRKYSHHNSDFYIP	160
CD16II_2	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYFHHNSDFHIP	160
CD16II_3	EDPIHLRCHSWKNTALHKVTTYLQ	NGKDRKYFHHNSDFHIP	160
*.*****.*** *****.***			
CD16I_1	KATLKDSGSYFCRGLVGSKNVSS	ETVNITITQGLAVSTIS	200
CD16I_4	KATLKDSGSYFCRGLVGSKNVSS	ETVNITITQGLAVSTIS	200
CD16I_3	KATLKDSGSYFCRGLVGSKNVSS	ETVNITITQGLAVSTIS	200
CD16I_2	KATLKDSGSYFCRGLVGSKNVSS	ETVNITITQGLAVSTIS	200
FCG3_HUMAN	KATLKDSGSYFCRGLFGSKNVSS	ETVNITITQGLAVSTIS	200
CD16II_1	KATLKDSGPFYFCRGLFGSKNVSS	ETVNTTITQGLAVSTIS	200
CD16II_4	KATLKDSGSYFCRGLFGSKNVSS	ETVNITITQGLAVSTIS	200
CD16II_2	KATLKDSGSYFCRGLVGSKNVSS	ETVNITIIQGLAVSTNS	200
CD16II_3	KATLKDSGSYFCRGLVGSKNVSS	ETVNITITQGLAVSTIS	200
*****.***.*** *****.***.***** *			

FIGURE 1

2/7

CD16I_1	SFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI-----	233
CD16I_4	SFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI-----	233
CD16I_3	SFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI-----	233
CD16I_2	SFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI-----	233
FCG3_HUMAN	SFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDW	240
CD16II_1	SFFPPGYQVSFCLAMVLLFAVDTGLYFSVKTNIRSSTRDW	240
CD16II_4	SFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDW	240
CD16II_2	SFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDW	240
CD16II_3	SFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDW	240
	** *****.*****	

CD16I_1	-----	233
CD16I_4	-----	233
CD16I_3	-----	233
CD16I_2	-----	233
FCG3_HUMAN	KDHKFKWRKDPQDK	254
CD16II_1	KDHKFKWRKDPQDK	254
CD16II_4	KDHKFKWRKDPQDK	254
CD16II_2	KDHKFKWRKDPQDK	254
CD16II_3	KDHKFKWRKDPQDK	254

FIGURE 1 - CONT.

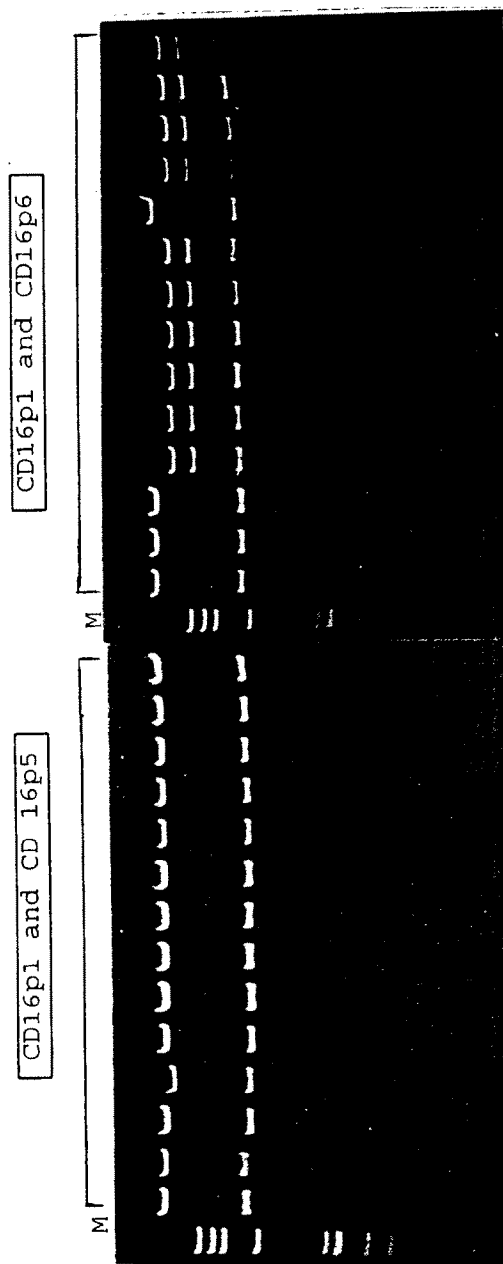
3/7

FIG. 2

Panel A: CD 16 Isoform-specific Oligonucleotide PC Primers:

	nt#	CD16p1	CD16P5 and CD16p6	nt#
Type I:	34	ATGTGGCAGCTGCTC.....GAGCAGTGGCAGCAG		836
		=====+=====		
Type II:	34	ATGTGGCAGCTGCTC.....GAGCAGTAGCAGCAG		836
		=====+=====		

Panel B: Restriction Digestion of CD 16 subtype with endonuclease DraI.



[illegible]

501
Four
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F e
hre
T
o p
W u
o
G t
701
765
Tou
F e l
Ghr
T p
W u O u
ro
t
600
700
5/7

-----g-----
-----a-----g-----t-----a-----
-----c-----c-----
CGGCTCCTACTTCTGACGGGGGCTTTTGGGAGTAAAAATGTGTCTTCAGAGACTGTGTAACATCACCATCAAGGTTTGGCAGTGTCAACCATCTCA

-----c-----
TCATTCTTTCCACCTGGGTACCAAGTCTCTTCTGTCTTGGTGATGGTACTCCTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAACATTC

-----c-----g-----

GAAGCTCAACAAGAGACTGGAGGACCATAAATTTAAATGGAGAAAGGACCCTCAAGACAAATGA

FIGURE 3 CONT.

6/7

FIG. 4

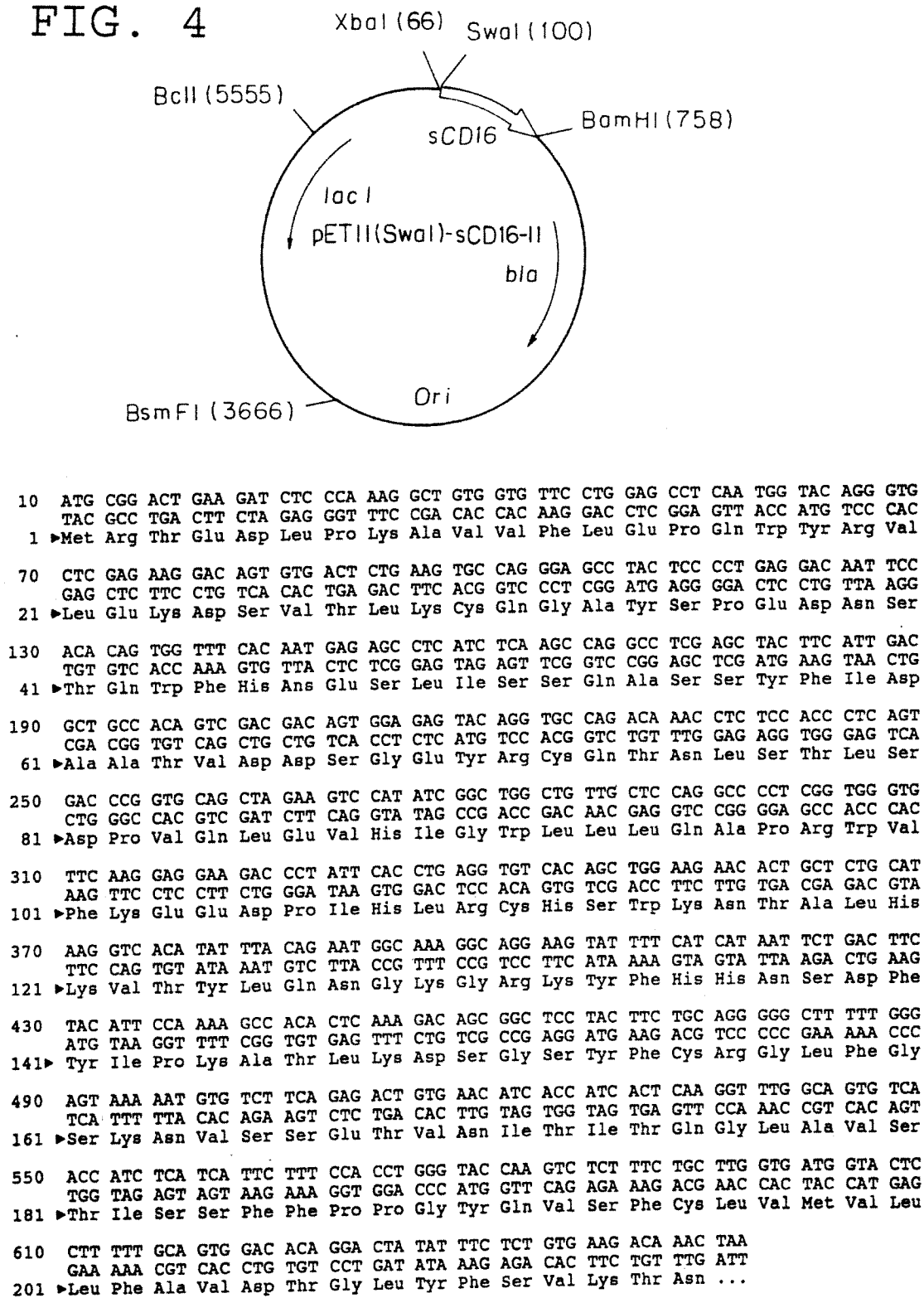
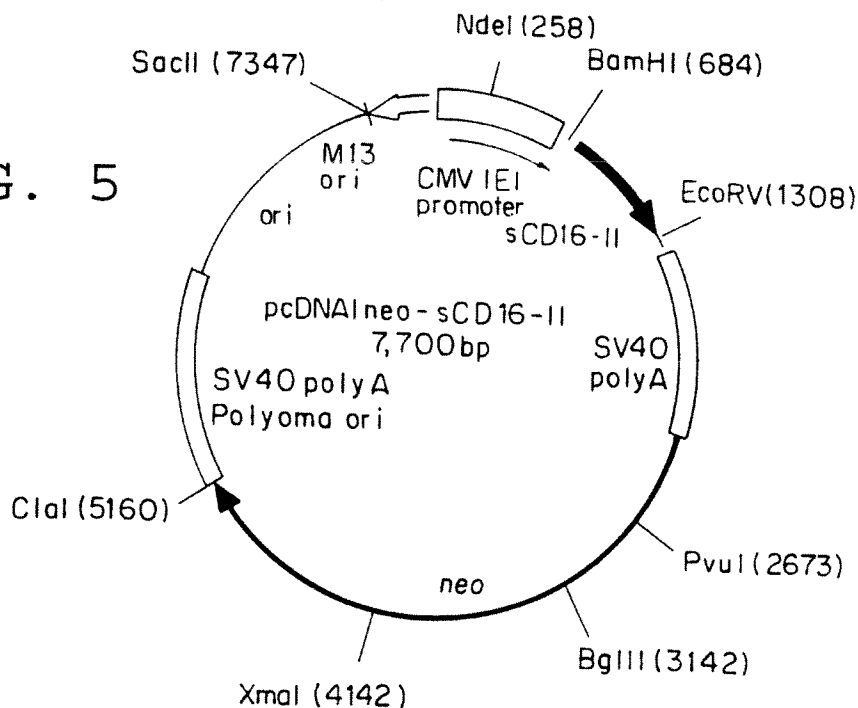


FIG. 5



BamHI

1 GGATCC ATG TGG CAG CTG CTC CTC CCA ACT GCT CTG CTA CTT CTA GTT TCA
 1 ▶ Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser

52 GCT GGC ATG CGG ACT GAA GAT CTC CCA AAG GCT GTG GTG TTC CTG GAG CCT
 16 ▶Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro

103 CAA TGG TAC AGG GTG CTC GAG AAG GAC AGT GTG ACT CTG AAG TGC CAG GGA
 33 ▶Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly

154 GTC TAC TCC CCT GAG GAC AAT TCC ACA CAG TGG TTT CAC AAT GAG AGC CTC
 50 ▶Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser Leu

205 ATC TCA AGC CAG GCC TCG AGC TAC TTC ATT GAC GCT GCC ACA GTC GAC GAC
 67 ▶Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val Asp Asp

256 AGT GGA GAG TAC AGG TGC CAG ACA AAC CTC TCC ACC CTC AGT GAC CCG GTG
 84 ▶Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser Asp Pro Val

307 CAG CTA GAA GTC CAT ATC GGC TGG CTG TTG CTC CAG GCC CCT CGG TGG GTG
 101 ▶Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala Pro Arg Trp Val

358 TTC AAG GAG GAA GAC CCT ATT CAC CTG AGG TGT CAC AGC TGG AAG AAC ACT
 118 ▶Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His Ser Trp Lys Asn Thr

409 GCT CTG CAT AAG GTC ACA TAT TTA CAG AAT GGC AAA GGC AGG AAG TAT TTT
 135 ▶Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe

460 CAT CAT AAT TCT GAC TTC TAC ATT CCA AAA GCC ACA CTC AAA GAC AGC GGC
 152 ▶His His Asn Ser Asp Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly

511 TCC TAC TTC TGC AGG GGG CTT TTT GGG AGT AAA AAT GTG TCT TCA GAG ACT
 169 ▶Ser Tyr Phe Cys Arg Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr

562 GTG AAC ATC ACC ATC ACT CAA GGT TTG GCA GTG TCA ACC ATC TCA TCA TTC
 186 ▶Val Asn Ile Thr Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe

EcoRV
 613 TTT TGA GAATTCGATATC
 203 ▶Phe ...